RAW SEQUENCE LISTING DATE: 12/26/2000
PATENT APPLICATION: US/09/659,860A TIME: 22:26:17

Input Set : A:\RTS-201.txt
Output Set: N:\CRF3\12262000\I659860A.raw

```
  3 <110> APPLICANT: Hong Zhang
  4       Andrew T. Watt
  6 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 7 EXPRESSION
  8 <130> FILE REFERENCE: RTS-0201
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/659,860A
C--> 10 <141> CURRENT FILING DATE: 2000-09-11
 10 <160> NUMBER OF SEQ ID NOS: 174
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 20
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Artificial Sequence
 18 <220> FEATURE:
 19 <223> OTHER INFORMATION: Antisense Oligonucleotide
 21 <400> SEQUENCE: 1
 22 tccgtcatcg ctcctcaggg                                                  20
 25 <210> SEQ ID NO: 2
 26 <211> LENGTH: 20
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Artificial Sequence
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: Antisense Oligonucleotide
 33 <400> SEQUENCE: 2
 34 atgcattctg ccccaagga                                                   20
 37 <210> SEQ ID NO: 3
 38 <211> LENGTH: 2309
 39 <212> TYPE: DNA
 40 <213> ORGANISM: Homo sapiens
 42 <220> FEATURE:
 43 <221> NAME/KEY: CDS
 44 <222> LOCATION: (44)...(955)
 46 <400> SEQUENCE: 3
 47 gagagactgt gccagtccca gccgccctac cgccgtggga acg atg gca gat gat       55
 48                                                 Met Ala Asp Asp
 49                                                   1
 51 cag ggc tgt att gaa gag cag ggg gtt gag gat tca gca aat gaa gat      103
 52 Gln Gly Cys Ile Glu Glu Gln Gly Val Glu Asp Ser Ala Asn Glu Asp
 53   5                  10                  15                  20
 55 tca gtg gat gct aag cca gac cgg tcc tcg ttt gta ccg tcc ctc ttc      151
 56 Ser Val Asp Ala Lys Pro Asp Arg Ser Ser Phe Val Pro Ser Leu Phe
 57                  25                  30                  35
 59 agt aag aag aag aaa aat gtc acc atg cga tcc atc aag acc acc cgg      199
 60 Ser Lys Lys Lys Lys Asn Val Thr Met Arg Ser Ile Lys Thr Thr Arg
 61              40                  45                  50
 63 gac cga gtg cct aca tat cag tac aac atg aat ttt gaa aag ctg ggc      247
 64 Asp Arg Val Pro Thr Tyr Gln Tyr Asn Met Asn Phe Glu Lys Leu Gly
 65          55                  60                  65
 67 aaa tgc atc ata ata aac aac aag aac ttt gat aaa gtg aca ggt atg      295
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68 Lys Cys Ile Ile Ile Asn Asn Lys Asn Phe Asp Lys Val Thr Gly Met
69      70                  75                  80
71 ggc gtt cga aac gga aca gac aaa gat gcc gag gcg ctc ttc aag tgc      343
72 Gly Val Arg Asn Gly Thr Asp Lys Asp Ala Glu Ala Leu Phe Lys Cys
73  85                  90                  95                  100
75 ttc cga agc ctg ggt ttt gac gtg att gtc tat aat gac tgc tct tgt      391
76 Phe Arg Ser Leu Gly Phe Asp Val Ile Val Tyr Asn Asp Cys Ser Cys
77                  105                 110                 115
79 gcc aag atg caa gat ctg ctt aaa aaa gct tct gaa gag gac cat aca      439
80 Ala Lys Met Gln Asp Leu Leu Lys Lys Ala Ser Glu Glu Asp His Thr
81              120                 125                 130
83 aat gcc gcc tgc ttc gcc tgc atc ctc tta agc cat gga gaa gaa aat      487
84 Asn Ala Ala Cys Phe Ala Cys Ile Leu Leu Ser His Gly Glu Glu Asn
85          135                 140                 145
87 gta att tat ggg aaa gat ggt gtc aca cca ata aag gat ttg aca gcc      535
88 Val Ile Tyr Gly Lys Asp Gly Val Thr Pro Ile Lys Asp Leu Thr Ala
89      150                 155                 160
91 cac ttt agg ggg gat aga tgc aaa acc ctt tta gag aaa ccc aaa ctc      583
92 His Phe Arg Gly Asp Arg Cys Lys Thr Leu Leu Glu Lys Pro Lys Leu
93 165                 170                 175                 180
95 ttc ttc att cag gct tgc cga ggg acc gag ctt gat gat ggc atc cag      631
96 Phe Phe Ile Gln Ala Cys Arg Gly Thr Glu Leu Asp Asp Gly Ile Gln
97                  185                 190                 195
99 gcc gac tcg ggg ccc atc aat gac aca gat gct aat cct cga tac aag      679
100 Ala Asp Ser Gly Pro Ile Asn Asp Thr Asp Ala Asn Pro Arg Tyr Lys
101             200                 205                 210
103 atc cca gtg gaa gct gac ttc ctc ttc gcc tat tcc acg gtt cca ggc      727
104 Ile Pro Val Glu Ala Asp Phe Leu Phe Ala Tyr Ser Thr Val Pro Gly
105         215                 220                 225
107 tat tac tcg tgg agg agc cca gga aga ggc tcc tgg ttt gtg caa gcc      775
108 Tyr Tyr Ser Trp Arg Ser Pro Gly Arg Gly Ser Trp Phe Val Gln Ala
109     230                 235                 240
111 ctc tgc tcc atc ctg gag gag cac gga aaa gac ctg gaa atc atg cag      823
112 Leu Cys Ser Ile Leu Glu Glu His Gly Lys Asp Leu Glu Ile Met Gln
113 245                 250                 255                 260
115 atc ctc acc agg gtg aat gac aga gtt gcc agg cac ttt gag tct cag      871
116 Ile Leu Thr Arg Val Asn Asp Arg Val Ala Arg His Phe Glu Ser Gln
117                 265                 270                 275
119 tct gat gac cca cac ttc cat gag aag aag cag atc ccc tgt gtg gtc      919
120 Ser Asp Asp Pro His Phe His Glu Lys Lys Gln Ile Pro Cys Val Val
121             280                 285                 290
123 tcc atg ctc acc aag gaa ctc tac ttc agt caa tag ccatatcagg          965
124 Ser Met Leu Thr Lys Glu Leu Tyr Phe Ser Gln
125         295                 300
127 ggtacattct agctgagaag caatgggtca ctcattaatg aatcacattt ttttatgctc  1025
129 ttgaaaatatt cagaaattct ccaggatttt aatttcagga aaatgtattg attcaacagg  1085
131 gaagaaacct tctggtgctg tcttttgttc tctgaatttt cagagacttt tttataatgt  1145
133 tattcatttg gtgactgtgt aacttttctt taagattaat ttttctttg tatgtctgtt  1205
135 accttgttaa tagacttaat acatgcaaca gaagtgactt ctggagaaag ctcatggctg  1265
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137 tgrccactgc aattggtggt aacagtggta gagtcatgtt tgcacttggc aaaaagaatc 1325
139 ccaatgtttg acaaaacaca gccaagggga tatttactgc tctttattgc agaatgtggg 1385
141 tattgagtgt gatttgaatg attttcatt ggcttagggc agattttcat gcaaaagttc 1445
143 tcatatgagt tagaggagaa aaagcttaat gattctgata tgtatccatc aggatccagt 1505
145 ctggaaaaca gaaaccattc tagggtgttc aacagaggga gtttaataca ggaaattgac 1565
147 ttacatagat gataaaagag aagccaaaca gcaagaagct gttaccacac ccagggctat 1625
149 gaggataatg ggaagaggtt tggtttcctg tgtccagtag tgggatcatc cagaggagct 1685
151 ggaaccatgg tggggctgc ctagtgggag ttaggaccac caatggattg tggaaaatgg 1745
153 agccatgaca agaacaaagc cactgactga gatggagtga gctgagacag ataagagaat 1805
155 accttgtctc acctatcctg ccctcacatc ttcrcaccagc acttactgc ccaggcctat 1865
157 ctggaagcca cctcaccaag gaccttggaa gaggaagggg cagtgaggca ggagaagaac 1925
159 aagaaatgga tgtaagcctg gcccataatg tgaacataag taatcactaa tgctcaacaa 1985
161 tttatccatt caatcatttg ttcattgggt tgtcagatag tctatgtatg tgtaaaacaa 2045
163 tctgtttigg ctttatgtgc aaaatctgtt atagctttaa aatatatctg gaacttttta 2105
165 gattatcca agccttattt tgagtaaata tttgtttact ttagttctat aagtgaggaa 2165
167 gagtttatgg caaagatttt tggcactttg ttttcaagat ggtgttatct tttgaattct 2225
169 tgataaatga ctgttttttt ctgcctaata gtaactggtt aaaaaacaaa tgttcatatt 2285
171 tattgattaa aaatgtggtt gctt 2309
174 <210> SEQ ID NO: 4
175 <211> LENGTH: 26
176 <212> TYPE: DNA
177 <213> ORGANISM: Artificial Sequence
179 <220> FEATURE:
180 <223> OTHER INFORMATION: PCR Primer
182 <400> SEQUENCE: 4 26
183 attggtggta acagtggtag agtcat
186 <210> SEQ ID NO: 5
187 <211> LENGTH: 20
188 <212> TYPE: DNA
189 <213> ORGANISM: Artificial Sequence
191 <220> FEATURE:
192 <223> OTHER INFORMATION: PCR Primer
194 <400> SEQUENCE: 5 20
195 cccttggctg tgttttgtca
198 <210> SEQ ID NO: 6
199 <211> LENGTH: 27
200 <212> TYPE: DNA
201 <213> ORGANISM: Artificial Sequence
203 <220> FEATURE:
204 <223> OTHER INFORMATION: PCR Probe
206 <400> SEQUENCE: 6 27
207 ttgcacttgg caaaaagaat cccaatg
210 <210> SEQ ID NO: 7
211 <211> LENGTH: 21
212 <212> TYPE: DNA
213 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:
216 <223> OTHER INFORMATION: PCR Primer
218 <400> SEQUENCE: 7

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219 caacqgattt ggtcgtattg g                                              21
222 <210> SEQ ID NO: 8
223 <211> LENGTH: 26
224 <212> TYPE: DNA
225 <213> ORGANISM: Artificial Sequence
227 <220> FEATURE:
228 <223> OTHER INFORMATION: PCR Primer
230 <400> SEQUENCE: 8
231 qqcaacaara tccactttac cagagt                                           26
234 <210> SEQ ID NO: 9
235 <211> LENGTH: 21
236 <212> TYPE: DNA
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <223> OTHER INFORMATION: PCR Probe
242 <400> SEQUENCE: 9
243 cgcctggtca ccaggqctgc t                                              21
246 <210> SEQ ID NO: 10
247 <211> LENGTH: 2006
248 <212> TYPE: DNA
249 <213> ORGANISM: Mus musculus
251 <220> FEATURE:
252 <221> NAME/KEY: CDS
253 <222> LOCATION: (474)...(1496)
255 <400> SEQUENCE: 10
256 agctcagtga ggctgatgtg tactgcacat ttaaaaaaaa aatcacagga attttcatac      60
258 aatgaataaa accacaacaa tacatgtaga attggcaggt qgaaaaqagc cagcaagggc     120
260 tcaaactaat cactcacttt ccctcttcaq catagttcaa ccuacagtag cacacttica     180
262 cctacaaatc ttaaagtagc tccatcaaat ctgcagtttt cacattattg aaaatgtctg     240
264 tcacataggt acaaatttag aatcatcaca ttatattaca tggctattct aggtcatcta     300
266 tagatcagat cttagactac agtgattgaa gttcttcgta cagccatcaa aaaqggacac     360
268 atgatcatta cctactgtta gctcacatct aaaggcatga aaaggtttcc ttttttttcaa    420
270 ctgacccaaa cactttaccc caatagtgcc aggttcccta tctgctgctt tga atg        476
271                                                          Met
272                                                           1
274 ttc aca gcc caa gtg ttc tca gag tcc ttt aca aaa act gag ttg ctg        524
275 Phe Thr Ala Gln Val Phe Ser Glu Ser Phe Thr Lys Thr Glu Leu Leu
276                 5                  10                  15
278 ccc tcg acc ctt gcg gag gac gga cgc tgc cgt ggg ctc ctg gcc gcc        572
279 Pro Ser Thr Leu Ala Glu Asp Gly Arg Cys Arg Gly Leu Leu Ala Ala
280         20                  25                  30
282 gcc gtg gga acg atg acc gat gat cag gac tgt gct gcg gag ctg gaa        620
283 Ala Val Gly Thr Met Thr Asp Asp Gln Asp Cys Ala Ala Glu Leu Glu
284     35                  40                  45
286 aag gtg gat tct tcc agc gaa gac gga gtt gac gcc aag cca gac cgc        668
287 Lys Val Asp Ser Ser Ser Glu Asp Gly Val Asp Ala Lys Pro Asp Arg
288  50                  55                  60                  65
290 tcc tct atc atc tcc tct att ctc ttg aag aag aag aga aat gcc tct       716
291 Ser Ser Ile Ile Ser Ser Ile Leu Leu Lys Lys Lys Arg Asn Ala Ser
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292                    70                  75                  80
294 gcg ggc ccc gtc agg acc ggc cgg gac cga gtg ccc act tat ctg tac      764
295 Ala Gly Pro Val Arg Thr Gly Arg Asp Arg Val Pro Thr Tyr Leu Tyr
296                 85                  90                  95
298 cgc atg gat ttc cag aag atg ggt aaa tgc atc atc ata aac aac aag      812
299 Arg Met Asp Phe Gln Lys Met Gly Lys Cys Ile Ile Ile Asn Asn Lys
300             100                 105                 110
302 aac ttc gac aaa gcg aca ggt atg gac gtc cgg aat ggg acg gac aaa      860
303 Asn Phe Asp Lys Ala Thr Gly Met Asp Val Arg Asn Gly Thr Asp Lys
304         115                 120                 125
306 gat gca ggg gcc ctc ttc aag tgc ttc caa aac ctg ggt ttt gaa gta      908
307 Asp Ala Gly Ala Leu Phe Lys Cys Phe Gln Asn Leu Gly Phe Glu Val
308 130                 135                 140                 145
310 acc gtc cac aat gac tgc tct tgt gca aag atg caa gat ctg ctt aga      956
311 Thr Val His Asn Asp Cys Ser Cys Ala Lys Met Gln Asp Leu Leu Arg
312                 150                 155                 160
314 aaa gcc tct gag gag gac cac agc aac tcg gcc tgc ttc gcc tgc gtc     1004
315 Lys Ala Ser Glu Glu Asp His Ser Asn Ser Ala Cys Phe Ala Cys Val
316             165                 170                 175
318 ctg ctg agc cac ggg gaa gag gac ctg att tac ggg aaa gat ggc gtg     1052
319 Leu Leu Ser His Gly Glu Glu Asp Leu Ile Tyr Gly Lys Asp Gly Val
320         180                 185                 190
322 aca ccc ata aag gat ctg aca gct cat ttt agg gga gac cga tgc aaa     1100
323 Thr Pro Ile Lys Asp Leu Thr Ala His Phe Arg Gly Asp Arg Cys Lys
324     195                 200                 205
326 acc ctg tta gag aaa ccc aaa ctc ttc ttc att cag gca tgc cga ggg     1148
327 Thr Leu Leu Glu Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Arg Gly
328 210                 215                 220                 225
330 acg gag ctc gac gat gga atc cag gct gac tcg ggg ccc atc aac gac     1196
331 Thr Glu Leu Asp Asp Gly Ile Gln Ala Asp Ser Gly Pro Ile Asn Asp
332                 230                 235                 240
334 att gac gct aat ccc cgc aac aag atc ccg gtg gaa gcc gac ttc ctc     1244
335 Ile Asp Ala Asn Pro Arg Asn Lys Ile Pro Val Glu Ala Asp Phe Leu
336             245                 250                 255
338 ttt gct tac tcc acg gtt cca ggt tat tac tca tgg agg aac cca ggg     1292
339 Phe Ala Tyr Ser Thr Val Pro Gly Tyr Tyr Ser Trp Arg Asn Pro Gly
340         260                 265                 270
342 aaa ggc tcc tgg ttt gtg cag gcc ctc tgc tcc atc ctg aat gag cat     1340
343 Lys Gly Ser Trp Phe Val Gln Ala Leu Cys Ser Ile Leu Asn Glu His
344     275                 280                 285
346 ggc aag gac ctc gag atc atg cag atc ctg acc agg gtg aac gac agg     1388
347 Gly Lys Asp Leu Glu Ile Met Gln Ile Leu Thr Arg Val Asn Asp Arg
348 290                 295                 300                 305
350 gtg gcc agg cac ttc gag tcc cag tct gat gat cca cgc ttc aac gag     1436
351 Val Ala Arg His Phe Glu Ser Gln Ser Asp Asp Pro Arg Phe Asn Glu
352                 310                 315                 320
354 aag aag cag atc ccg tgt atg gtg tcc atg ctc acc aaa gag ctg tac     1484
355 Lys Lys Gln Ile Pro Cys Met Val Ser Met Leu Thr Lys Glu Leu Tyr
356             325                 330                 335
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Input Set : A:\RTS-201.txt
Output Set: N:\CRF3\12262000\I659860A.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date